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TITLE A TODA LATTICE MODEL OF DNA

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A TODA LATTICE MODEL OF DNA

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ABSTRACT

The role of anharmonicity in the dynamics of DNA at biological temperatures is currently discussed by many authors. Here results obtained by a Toda lattice model of the molecule in Refs. 1-4 are summarized.

Introduction

In recent years the possibility that anharmonic excitations could play a role in the dynamics of DNA has been considered by several authors 1-12. Further references are given in Muto et al. 1. It has been suggested that solitons may be generated thermally at biological temperatures. However, this question is far from being settled at the present time and can be described as controversial 13-15, e.g.. The denaturation of the DNA double helix has been investigated by statistical mechanics methods and by dynamical simulation 16,17. Here the potential for the hydrogen bond in each base pair is approximated by a Morse potential.

In the present paper we describe the Toda lattice model of DNA introduced in Refs. 1,2. Temperature enters via the initial conditions and through a perturbation of the dynamical equations. The model is refined by introduction of transversal motion of the Toda lattice³ and by transversal coupling of two lattices in the hydrogen bonds present in the base pairs⁴. Using Lennard-Jones potentials to model these bonds we are able to obtain results concerning the open states of DNA at biological temperatures.

The Toda Lattice Model

The Toda lattice 18,19 consists of N masses (each of mass m) with longitudinal displacements from equidistant equilibrium positions given by $y_n(t)$ (n = 1,2,...,N) as a function of time.

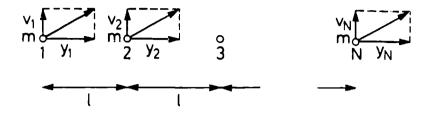


Figure 1. Lattice with longitudinal and transversal degrees of freedom.

Fig. 1 illustrates the case where both longitudinal and transversal displacements, given by $y_n(t)$ and $v_n(t)$ respectively, $n=1,2,\cdots,N$, are possible. ℓ is the lattice constant. The masses are connected to their nearest neighbours with nonlinear springs of potential $V(y_{n+1}-y_n)$ when only longitudinal motion is allowed. In this case Newton's second law becomes

$$m\ddot{y}_{n} = V'(y_{n+1} - y_{n}) - V'(y_{n} - y_{n-1})$$
, $n = 1, \dots, N$ (1a)

where the dot indicates a time derivative and the prime indicates a derivative with respect to the argument. For the Toda lattice the nonlinear spring potential is

$$V(y_{n+1} - y_n) = \frac{a}{b} \exp \left[-b(y_{n+1} - y_n)\right] + a(y_{n+1} - y_n)$$
 (2)

where a and b are arbitrary parameters.

In the model each mass represents a single base pair, and the nonlinear spring represents the potential between adjacent base pairs (of both DNA strands of the double helix in the simple model).

The most realistic potential function between the base pairs is the generalized van der Waals function

$$\tilde{V}(Y_{n+1} - Y_n) = \frac{A}{(\ell - Y_{n+1} - Y_n)^p} - \frac{B}{(\ell + Y_{n+1} - Y_n)^q}$$
 (3)

Equating polynomial coefficients of V and \tilde{V} up to third order gives b = $(p+g+3)/\ell$ where $\ell=3.4$ Å. With p=12 and $q=6^{20,21}$ we get

$$b = 6.18 \times 10^{10} \text{ m}^{-1}$$
 (4)

Near the minimum $(y_{n+1}-y_n=0)$, Eq. 2 reduces to a harmonic potential with a spring force constant k=ab. Experimental measurements of the sound velocity of DNA $(\ell\sqrt{k/m}=1.69\times10^3~m/s)^{22}$ then require

$$a = 5.13 \times 10^{-10} \text{ N}$$
, (5)

m being the mass of the base pair, m = 1.28 \times 10⁻²⁶ kg^{22,23}.

In a cyclic arrangement of the N masses, corresponding to a closed DNA molecule, we use the periodic boundary conditions

$$y_{n+N}(t) = y_n(t) . (6a)$$

The advantage of the Toda lattice model is its integrability. As first pointed out by Flaschka 24 , 25 the equations of motion, Eq. 1a, can after a transformation - be expressed in a Lax formalism. Using this re-

sult the initial value problem for the infinite lattice can be solved exactly $^{24-26}$. In particular, solitons are specified by bound states for which the corresponding eigenvalues are greater than +1 or less than - 1^{27} , 28 . A simple and effective method for counting the number of solitons 29 has been described and used in Refs. 1.2, as we shall see in the following sections.

Thermalization of the Simple Model

In order to thermalize the system we first assume 1 that there is a total energy approximately equal to $k_B T$ initially in the system. (Here k_B is the Boltzmann constant and T is the absolute temperature.) This is clearly an approximation since, at thermal equilibrium, the average kinetic energy is equal to $\frac{1}{2}k_B T$, while the potential energy differs from $\frac{1}{2}k_B T$ in a nonlinear system. Assuming, nevertheless, that all masses have gaussian random displacements from their equilibrium positions and gaussian random velocities such that the total energy is equally shared between kinetic and potential energy we get the number of solitons, N_S , versus temperature shown in Fig. 2. Here the soliton counter is applied

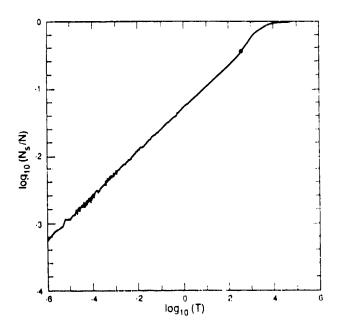


Figure 2. Logarithm of N_S/N versus logarithm of T measured in K. Kinetic and potential energies equal to $\frac{1}{2}k_BT$. The bullet (\bullet) indicates biological temperature.

directly to the initial data for the unperturbed Toda lattice. The point indicated by bullet (•) corresponds to T = 310 K and gives $N_{\rm S}/N$ = 0.35. At high temperatures $N_{\rm S} \rightarrow N$ as expected. At lower temperatures (T < 100 K) the number of solitons is proportional to $T^{1/3}$. Almost similar results were found when the initial energy of the system was either completely kinetic or completely potential. In an unpublished paper 30 Schneider and Stoll, using the ideal soliton gas approximation, also found a $T^{1/3}$ -law

for N_S . However, according to Bolterauer and Opper 31 their analysis contains a mistake in the consideration of canonically conjugate variables. Mertens and Büttner 32,33 , using action-angle variables for the Toda lattice, find $N_S \propto T$ at low temperatures. The discrepancy may be due to the fact that not only solitons, but also anharmonic phonons are counted 32,33 .

A second approach to thermalization consists in describing the interaction of the DNA molecule with a thermal reservoir at a finite temperature through Langevin equations 4, e.g.. Thus a damping force and a noise force

$$F_n = - m A \dot{y}_n + \eta_n(t) \tag{7}$$

are added on the right-hand side of the dynamical equations, Eq. 1a. Here A is the damping coefficient and $\eta_{\Pi}(t)$ is the random force with correlation function

$$\langle \eta_n(t) \eta_n'(b') \rangle = 2m A k_B T \delta_{nn'} \delta(t-t')$$
 (8)

in the case of white noise. The coefficient, $2m\,A\,k_B\,T$, in front of the Kronecker delta, δ_{nn} , and Dirac's delta function, δ (t-t'), is chosen in accordance with fluctuation-dissipation theorem³⁴. Assuming that the damping is simply due to the viscosity of the water surrounding the DNA-molecule representative values of the damping coefficient are A = $0.85\,\sqrt{ab/m}$ (corresponding to approximately critical damping) and A = $0.85\,\sqrt{ab/m}$ (corresponding to overdamping). By integrating the perturbed dy-

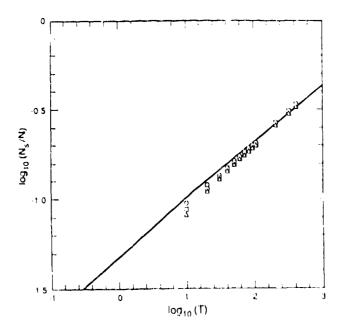


Figure 3. Logarithm of N_g/N versus logarithm of T measured in K for damping coefficient $A/\sqrt{ab/m}=5$, 3, 0.85 indicated by circles, squares and triangles. Full curve obtained by thermalized initial data: Kinetic energy equal to k_BT , potential energy equal to 0.

namical equations, Eqs. 1a and 7, until thermal equilibrium has been reached and then using the soliton counter on the resulting solution we obtain curves for $N_{\rm S}$ versus T as shown in Fig. 3. For different values of α we get good agreement with the results obtained by the first approximation where the thermal fluctuations are present only in (the kinetic energy of) the initial data. Thus $N_{\rm S}$ = 0.31 N at T = 310 K and $N_{\rm S}$ \propto $T^{1/3}$ for T < 100 K.

Thus both of the two thermalization approaches demonstrate that a significant number of solitons, approximately 1/3 of the number of base pairs, are generated at biological temperature.

Toda Lattice with Transversal Degree of Freedom

In order to refine the model we first introduce a transversal degree of freedom³. As a result we get the dynamical equations

$$m\dot{y}_{n} = -V'(r_{n}) \frac{\partial r_{n}}{\partial y_{n}} - V'(r_{n-1}) \frac{\partial r_{n-1}}{\partial y_{n}}$$
 (1b)

$$mv_{n} = -V'(r_{n}) \frac{\partial r_{n}}{\partial v_{n}} - V'(r_{n-1}) \frac{\partial r_{n-1}}{\partial v_{n}}.$$
 (1c)

Here the potential V is still given by Eq. 2, and

$$r_{n} = \sqrt{(\ell + y_{n+1} - y_{n})^{2} + (v_{n+1} - v_{n})^{2}} - \ell . \tag{9}$$

Periodic boundary conditions for longitudinal and transverse displacements are

$$y_{N+n}(t) = y_n(t)$$
 , $v_{N+n}(t) = v_n(t)$. (6b)

In order to derive continuum approximations for the lattice equations, Eqs. 1b-c, we follow Collins, Rosenau, and Hyman and Rosenau $^{35-37}$ who showed that

$$T(f_{n+1}) - 2T(f_n) + T(f_{n-1}) \rightarrow \left(1 - \frac{\ell^2}{12} \frac{\partial^2}{\partial x^2}\right)^{-1} \ell^2 \frac{\partial^2}{\partial x^2} T(f)$$
, (10)

where T is a nonlinear function of $f_n(t) \rightarrow f(x,t) \equiv f(n\ell,t)$ in the continuum limit $n \rightarrow \infty$, $\ell \rightarrow 0$, $n\ell = x$. In the case where the longitudinal strain $u_n \equiv (y_{n+1} - y_n)/\ell$ is of the same order of magnitude as the transversal strain $u_n \equiv (v_{n+1} - v_n)/\ell$ we obtain (see also Ref. 38)

$$\frac{\rho}{a} u_{tt} = \beta u_{xx} - \frac{\beta^2}{2} (u^2)_{xx} + \frac{\beta}{2} (w^2)_{xx} + \frac{\rho}{a} \frac{\ell^2}{12} u_{xxtt}$$
 (11a)

$$\frac{\rho}{a} w_{tt} = \beta(uw)_{xx} + \frac{\rho}{a} \frac{\ell^2}{12} w_{xx}tt$$
 (11b)

in the Boussinesq approximation where

$$V(r_n) \propto \frac{a}{b} \left[\frac{(br_n)^2}{2} - \frac{(br_n)^3}{6} \right] .$$
 (12)

Here $\rho \equiv m/\ell = 3.77 \times 10^{-15}$ kg/m and $\beta \equiv \ell b = 21$ in the case of DNA. Exact travelling wave solutions to Eq. 11 of the form

$$w = \pm \sqrt{2 + \beta} u \mp \frac{\sqrt{2+\beta}}{1+\beta}$$
, (13)

for infinite and finite length of the molecule, are found in Refs. 3 and 39. The numerical simulations of this hybrid travelling wave (with initial velocity s = 1.5) is shown in Figs. 4 and 5 in the discrete case, Eqs. 1b-c and the continuum case, Eqs. 11a-b. In the discrete case rather

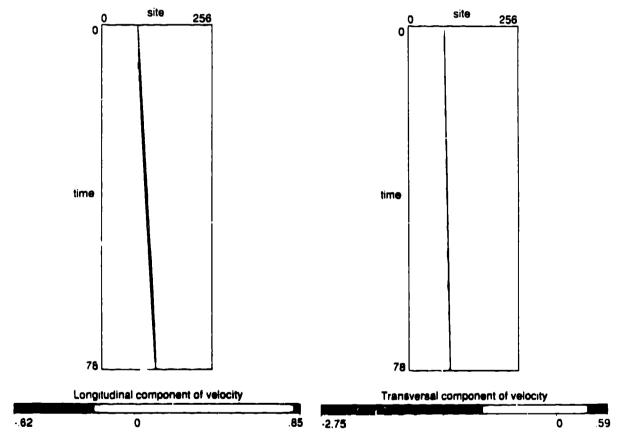


Figure 4. Grey-scale plot of (a) longitudinal and (b) transversal velocities, $\dot{y}_n(t)$ and $\dot{v}_n(t)$, versus site n and normalized time t. Dispersion occurs at t = 3.

Etrong dispersion occurs while in the continuum case blow-up occurs in the longitudinal component after a finite time. (In the latter case the hybrid wave remains stable for smaller values of the initial velocity $s \ (s > 1)$.)

We conclude that despite the fact that the hybrid wave may not be stable the longitudinal soliton-like excitation travels along the molecule for extended periods of time, also in the presence of a transversal decree of freedom.

Two Coupled Toda Lattices

Finally, we consider 4 two strands of DNA coupled together via the hydrogen bonds in the base pairs as shown in Fig. 6. The potentials

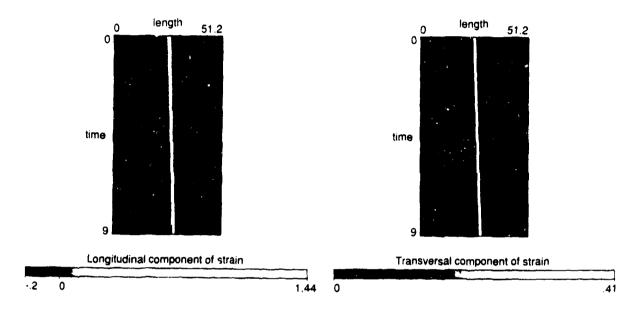


Figure 5. Grey-scale plot of (a) longitudinal and (b) transversal strains, u(x,t) and w(x,t), versus normalized distance x and time t. Blow-up (black lines) occurs in the longitudinal component at t=9.

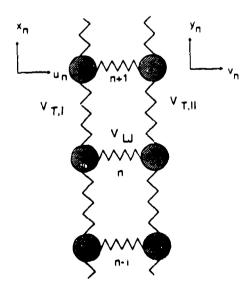


Figure 6. DNA double helix. Two identical Toda chains are connected by Lennard-Jones potentials representing the hydrogen bonds between the two strands.

along the strands, $V_{T,I}$ and $V_{T,II}$, are Toda potentials of the form of Eq. 2. The hydrogen bonds are modelled by Lennard-Jones potentials, V_{LJ} , of the form of Eq. 3 with p=12 and q=6. The main result of the investigation is shown in Fig. 7 illustrating the averaged life-time of the open states versus temperature T. The open state of a hydrogen bond

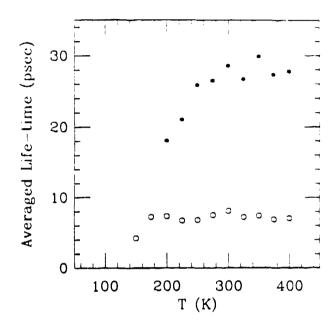


Figure 7. Averaged life-time of open states versus temperature T. Bin 3 - 17 psec: open symbols.
Bin > 18 psec: stars.

occurs when the transversal distance between the bases in a pair is bigger than $4 \, \text{\AA}$. To obtain Fig. 7 we divide the open states in three bins. The first bin contains open states with a life-time shorter than 3 psec. These states are not considered in the calculations of the averaged life-times. The second bin contains open states with life-times 3-17 psec. The averaged values of this group are shown in Fig. 7 as open symbols. Finally, the third bin contains the open states with a life-time longer than 18 psec. These averaged values are plotted by stars. The figure clearly shows that for temperatures larger than $T=250 \, \text{K}$, the presence of open states which last for more than 20 psec is significant.

Thus we conclude that anharmonicity may play a role in the DNA denaturation.

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